

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Ullrich, Axel
Risau, Werner
Millauer, Birgit
Gazit, Aviv
Levitzki, Alex
- (ii) TITLE OF INVENTION: Flk-1 Is A Receptor For Vascular
Endothelial Growth Factor
- (iii) NUMBER OF SEQUENCES: 6
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Pennie & Edmonds
 - (B) STREET: 1155 Avenue of the Americas
 - (C) CITY: New York
 - (D) STATE: New York
 - (E) COUNTRY: U.S.A.
 - (F) ZIP: 10036-2711
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/193,829
 - (B) FILING DATE: 09-FEB-1994
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Coruzzi, Laura A.
 - (B) REGISTRATION NUMBER: 30,742
 - (C) REFERENCE/DOCKET NUMBER: 7683-060
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (212)790-9090
 - (B) TELEFAX: (212)869-9741
 - (C) TELEX: 66141 PENNIE

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5470 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: DNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 286..4386

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TATAGGGCGA ATTGGGTACG GGACCCCCCT CGAGGTCGAC GGTATCGATA AGCTTGATAT	60
CGAATTCGGG CCCAGACTGT GTCCCGCAGC CGGGATAACC TGGCTGACCC GATTCCGCGG	120
ACACCGCTGA CAGCCGCGGC TGGAGCCAGG GCGCCGGTGC CCCGCGCTCT CCCCAGTCTT	180
GCGCTGCGGG GGCCATACCG CCTCTGTGAC TTCTTTGCGG GCCAGGGACG GAGAAGGAGT	240
CTGTGCCTGA GAAACTGGGC TCTGTGCCCA GGCGCGAGGT GCAGG ATG GAG AGC	294
Met Glu Ser	
1	
AAG GCG CTG CTA GCT GTC GCT CTG TGG TTC TGC GTG GAG ACC CGA GCC	342
Lys Ala Leu Leu Ala Val Ala Leu Trp Phe Cys Val Glu Thr Arg Ala	
5 10 15	
GCC TCT GTG GGT TTG ACT GGC GAT TTT CTC CAT CCC CCC AAG CTC AGC	390
Ala Ser Val Gly Leu Thr Gly Asp Phe Leu His Pro Pro Lys Leu Ser	
20 25 30 35	
ACA CAG AAA GAC ATA CTG ACA ATT TTG GCA AAT ACA ACC CTT CAG ATT	438
Thr Gln Lys Asp Ile Leu Thr Ile Leu Ala Asn Thr Thr Leu Gln Ile	
40 45 50	
ACT TGC AGG GGA CAG CGG GAC CTG GAC TGG CTT TGG CCC AAT GCT CAG	486
Thr Cys Arg Gly Gln Arg Asp Leu Asp Trp Leu Trp Pro Asn Ala Gln	
55 60 65	
CGT GAT TCT GAG GAA AGG GTA TTG GTG ACT GAA TGC GGC GGT GGT GAC	534
Arg Asp Ser Glu Glu Arg Val Leu Val Thr Glu Cys Gly Gly Gly Asp	
70 75 80	
AGT ATC TTC TGC AAA ACA CTC ACC ATT CCC AGG GTG GTT GGA AAT GAT	582
Ser Ile Phe Cys Lys Thr Leu Thr Ile Pro Arg Val Val Gly Asn Asp	
85 90 95	
ACT GGA GCC TAC AAG TGC TCG TAC CGG GAC GTC GAC ATA GCC TCC ACT	630
Thr Gly Ala Tyr Lys Cys Ser Tyr Arg Asp Val Asp Ile Ala Ser Thr	
100 105 110 115	
GTT TAT GTC TAT GTT CGA GAT TAC AGA TCA CCA TTC ATC GCC TCT GTC	678
Val Tyr Val Tyr Val Arg Asp Tyr Arg Ser Pro Phe Ile Ala Ser Val	
120 125 130	
AGT GAC CAG CAT GGC ATC GTG TAC ATC ACC GAG AAC AAG AAC AAA ACT	726
Ser Asp Gln His Gly Ile Val Tyr Ile Thr Glu Asn Lys Asn Lys Thr	
135 140 145	
GTG GTG ATC CCC TGC CGA GGG TCG ATT TCA AAC CTC AAT GTG TCT CTT	774
Val Val Ile Pro Cys Arg Gly Ser Ile Ser Asn Leu Asn Val Ser Leu	
150 155 160	
TGC GCT AGG TAT CCA GAA AAG AGA TTT GTT CCG GAT GGA AAC AGA ATT	822
Cys Ala Arg Tyr Pro Glu Lys Arg Phe Val Pro Asp Gly Asn Arg Ile	
165 170 175	
TCC TGG GAC AGC GAG ATA GGC TTT ACT CTC CCC AGT TAC ATG ATC AGC	870
Ser Trp Asp Ser Glu Ile Gly Phe Thr Leu Pro Ser Tyr Met Ile Ser	
180 185 190 195	

TAT GCC GGC ATG GTC TTC TGT GAG GCA AAG ATC AAT GAT GAA ACC TAT Tyr Ala Gly Met Val Phe Cys Glu Ala Lys Ile Asn Asp Glu Thr Tyr 200 205 210	918
CAG TCT ATC ATG TAC ATA GTT GTG GTT GTA GGA TAT AGG ATT TAT GAT Gln Ser Ile Met Tyr Ile Val Val Val Gly Tyr Arg Ile Tyr Asp 215 220 225	966
GTG ATT CTG AGC CCC CCG CAT GAA ATT GAG CTA TCT GCC GGA GAA AAA Val Ile Leu Ser Pro Pro His Glu Ile Glu Leu Ser Ala Gly Glu Lys 230 235 240	1014
CTT GTC TTA AAT TGT ACA GCG AGA ACA GAG CTC AAT GTG GGG CTT GAT Leu Val Leu Asn Cys Thr Ala Arg Thr Glu Leu Asn Val Gly Leu Asp 245 250 255	1062
TTC ACC TGG CAC TCT CCA CCT TCA AAG TCT CAT CAT AAG AAG ATT GTA Phe Thr Trp His Ser Pro Pro Ser Lys Ser His His Lys Lys Ile Val 260 265 270 275	1110
AAC CGG GAT GTG AAA CCC TTT CCT GGG ACT GTG GCG AAG ATG TTT TTG Asn Arg Asp Val Lys Pro Phe Pro Gly Thr Val Ala Lys Met Phe Leu 280 285 290	1158
AGC ACC TTG ACA ATA GAA AGT GTG ACC AAG AGT GAC CAA GGG GAA TAC Ser Thr Leu Thr Ile Glu Ser Val Thr Lys Ser Asp Gln Gly Glu Tyr 295 300 305	1206
ACC TGT GTA GCG TCC AGT GGA CGG ATG ATC AAG AGA AAT AGA ACA TTT Thr Cys Val Ala Ser Ser Gly Arg Met Ile Lys Arg Asn Arg Thr Phe 310 315 320	1254
GTC CGA GTT CAC ACA AAG CCT TTT ATT GCT TTC GGT AGT GGG ATG AAA Val Arg Val His Thr Lys Pro Phe Ile Ala Phe Gly Ser Gly Met Lys 325 330 335	1302
TCT TTG GTG GAA GCC ACA GTG GGC AGT CAA GTC CGA ATC CCT GTG AAG Ser Leu Val Glu Ala Thr Val Gly Ser Gln Val Arg Ile Pro Val Lys 340 345 350 355	1350
TAT CTC AGT TAC CCA GCT CCT GAT ATC AAA TGG TAC AGA AAT GGA AGG Tyr Leu Ser Tyr Pro Ala Pro Asp Ile Lys Trp Tyr Arg Asn Gly Arg 360 365 370	1398
CCC ATT GAG TCC AAC TAC ACA ATG ATT GTT GGC GAT GAA CTC ACC ATC Pro Ile Glu Ser Asn Tyr Thr Met Ile Val Gly Asp Glu Leu Thr Ile 375 380 385	1446
ATG GAA GTG ACT GAA AGA GAT GCA GGA AAC TAC ACG GTC ATC CTC ACC Met Glu Val Thr Glu Arg Asp Ala Gly Asn Tyr Thr Val Ile Leu Thr 390 395 400	1494
AAC CCC ATT TCA ATG GAG AAA CAG AGC CAC ATG GTC TCT CTG GTT GTG Asn Pro Ile Ser Met Glu Lys Gln Ser His Met Val Ser Leu Val Val 405 410 415	1542
AAT GTC CCA CCC CAG ATC GGT GAG AAA GCC TTG ATC TCG CCT ATG GAT Asn Val Pro Pro Gln Ile Gly Glu Lys Ala Leu Ile Ser Pro Met Asp 420 425 430 435	1590
TCC TAC CAG TAT GGG ACC ATG CAG ACA TTG ACA TGC ACA GTC TAC GCC	1638

Ser	Tyr	Gln	Tyr	Gly	Thr	Met	Gln	Thr	Leu	Thr	Cys	Thr	Val	Tyr	Ala	
				440					445						450	
AAC	CCT	CCC	CTG	CAC	CAC	ATC	CAG	TGG	TAC	TGG	CAG	CTA	GAA	GAA	GCC	1686
Asn	Pro	Pro	Leu	His	His	Ile	Gln	Trp	Tyr	Trp	Gln	Leu	Glu	Glu	Ala	
			455					460					465			
TGC	TCC	TAC	AGA	CCC	GGC	CAA	ACA	AGC	CCG	TAT	GCT	TGT	AAA	GAA	TGG	1734
Cys	Ser	Tyr	Arg	Pro	Gly	Gln	Thr	Ser	Pro	Tyr	Ala	Cys	Lys	Glu	Trp	
		470					475					480				
AGA	CAC	GTG	GAG	GAT	TTC	CAG	GGG	GGA	AAC	AAG	ATC	GAA	GTC	ACC	AAA	1782
Arg	His	Val	Glu	Asp	Phe	Gln	Gly	Gly	Asn	Lys	Ile	Glu	Val	Thr	Lys	
	485					490					495					
AAC	CAA	TAT	GCC	CTG	ATT	GAA	GGA	AAA	AAC	AAA	ACT	GTA	AGT	ACG	CTG	1830
Asn	Gln	Tyr	Ala	Leu	Ile	Glu	Gly	Lys	Asn	Lys	Thr	Val	Ser	Thr	Leu	
500					505					510					515	
GTC	ATC	CAA	GCT	GCC	AAC	GTG	TCA	GCG	TTG	TAC	AAA	TGT	GAA	GCC	ATC	1878
Val	Ile	Gln	Ala	Ala	Asn	Val	Ser	Ala	Leu	Tyr	Lys	Cys	Glu	Ala	Ile	
				520					525						530	
AAC	AAA	GCG	GGA	CGA	GGA	GAG	AGG	GTC	ATC	TCC	TTC	CAT	GTG	ATC	AGG	1926
Asn	Lys	Ala	Gly	Arg	Gly	Glu	Arg	Val	Ile	Ser	Phe	His	Val	Ile	Arg	
			535					540					545			
GGT	CCT	GAA	ATT	ACT	GTG	CAA	CCT	GCT	GCC	CAG	CCA	ACT	GAG	CAG	GAG	1974
Gly	Pro	Glu	Ile	Thr	Val	Gln	Pro	Ala	Ala	Gln	Pro	Thr	Glu	Gln	Glu	
		550					555						560			
AGT	GTG	TCC	CTG	TTG	TGC	ACT	GCA	GAC	AGA	AAT	ACG	TTT	GAG	AAC	CTC	2022
Ser	Val	Ser	Leu	Leu	Cys	Thr	Ala	Asp	Arg	Asn	Thr	Phe	Glu	Asn	Leu	
	565					570					575					
ACG	TGG	TAC	AAG	CTT	GGC	TCA	CAG	GCA	ACA	TCG	GTC	CAC	ATG	GGC	GAA	2070
Thr	Trp	Tyr	Lys	Leu	Gly	Ser	Gln	Ala	Thr	Ser	Val	His	Met	Gly	Glu	
580					585					590					595	
TCA	CTC	ACA	CCA	GTT	TGC	AAG	AAC	TTG	GAT	GCT	CTT	TGG	AAA	CTG	AAT	2118
Ser	Leu	Thr	Pro	Val	Cys	Lys	Asn	Leu	Asp	Ala	Leu	Trp	Lys	Leu	Asn	
				600					605					610		
GGC	ACC	ATG	TTT	TCT	AAC	AGC	ACA	AAT	GAC	ATC	TTG	ATT	GTG	GCA	TTT	2166
Gly	Thr	Met	Phe	Ser	Asn	Ser	Thr	Asn	Asp	Ile	Leu	Ile	Val	Ala	Phe	
			615					620					625			
CAG	AAT	GCC	TCT	CTG	CAG	GAC	CAA	GGC	GAC	TAT	GTT	TGC	TCT	GCT	CAA	2214
Gln	Asn	Ala	Ser	Leu	Gln	Asp	Gln	Gly	Asp	Tyr	Val	Cys	Ser	Ala	Gln	
		630					635					640				
GAT	AAG	AAG	ACC	AAG	AAA	AGA	CAT	TGC	CTG	GTC	AAA	CAG	CTC	ATC	ATC	2262
Asp	Lys	Lys	Thr	Lys	Lys	Arg	His	Cys	Leu	Val	Lys	Gln	Leu	Ile	Ile	
	645					650					655					
CTA	GAG	CGC	ATG	GCA	CCC	ATG	ATC	ACC	GGA	AAT	CTG	GAG	AAT	CAG	ACA	2310
Leu	Glu	Arg	Met	Ala	Pro	Met	Ile	Thr	Gly	Asn	Leu	Glu	Asn	Gln	Thr	
660					665					670					675	
ACA	ACC	ATT	GGC	GAG	ACC	ATT	GAA	GTG	ACT	TGC	CCA	GCA	TCT	GGA	AAT	2358
Thr	Thr	Ile	Gly	Glu	Thr	Ile	Glu	Val	Thr	Cys	Pro	Ala	Ser	Gly	Asn	

680	685	690	
CCT ACC CCA CAC ATT ACA TGG TTC AAA GAC AAC GAG ACC CTG GTA GAA Pro Thr Pro His Ile Thr Trp Phe Lys Asp Asn Glu Thr Leu Val Glu 695 700 705			2406
GAT TCA GGC ATT GTA CTG AGA GAT GGG AAC CGG AAC CTG ACT ATC CGC Asp Ser Gly Ile Val Leu Arg Asp Gly Asn Arg Asn Leu Thr Ile Arg 710 715 720			2454
AGG GTG AGG AAG GAG GAT GGA GGC CTC TAC ACC TGC CAG GCC TGC AAT Arg Val Arg Lys Glu Asp Gly Gly Leu Tyr Thr Cys Gln Ala Cys Asn 725 730 735			2502
GTC CTT GGC TGT GCA AGA GCG GAG ACG CTC TTC ATA ATA GAA GGT GCC Val Leu Gly Cys Ala Arg Ala Glu Thr Leu Phe Ile Ile Glu Gly Ala 740 745 750 755			2550
CAG GAA AAG ACC AAC TTG GAA GTC ATT ATC CTC GTC GGC ACT GCA GTG Gln Glu Lys Thr Asn Leu Glu Val Ile Ile Leu Val Gly Thr Ala Val 760 765 770			2598
ATT GCC ATG TTC TTC TGG CTC CTT CTT GTC ATT GTC CTA CGG ACC GTT Ile Ala Met Phe Phe Trp Leu Leu Leu Val Ile Val Leu Arg Thr Val 775 780 785			2646
AAG CGG GCC AAT GAA GGG GAA CTG AAG ACA GGC TAC TTG TCT ATT GTC Lys Arg Ala Asn Glu Gly Glu Leu Lys Thr Gly Tyr Leu Ser Ile Val 790 795 800			2694
ATG GAT CCA GAT GAA TTG CCC TTG GAT GAG CGC TGT GAA CGC TTG CCT Met Asp Pro Asp Glu Leu Pro Leu Asp Glu Arg Cys Glu Arg Leu Pro 805 810 815			2742
TAT GAT GCC AGC AAG TGG GAA TTC CCC AGG GAC CGG CTG AAA CTA GGA Tyr Asp Ala Ser Lys Trp Glu Phe Pro Arg Asp Arg Leu Lys Leu Gly 820 825 830 835			2790
AAA CCT CTT GGC CGC GGT GCC TTC GGC CAA GTG ATT GAG GCA GAC GCT Lys Pro Leu Gly Arg Gly Ala Phe Gly Gln Val Ile Glu Ala Asp Ala 840 845 850			2838
TTT GGA ATT GAC AAG ACA GCG ACT TGC AAA ACA GTA GCC GTC AAG ATG Phe Gly Ile Asp Lys Thr Ala Thr Cys Lys Thr Val Ala Val Lys Met 855 860 865			2886
TTG AAA GAA GGA GCA ACA CAC AGC GAG CAT CGA GCC CTC ATG TCT GAA Leu Lys Glu Gly Ala Thr His Ser Glu His Arg Ala Leu Met Ser Glu 870 875 880			2934
CTC AAG ATC CTC ATC CAC ATT GGT CAC CAT CTC AAT GTG GTG AAC CTC Leu Lys Ile Leu Ile His Ile Gly His His Leu Asn Val Val Asn Leu 885 890 895			2982
CTA GGC GCC TGC ACC AAG CCG GGA GGG CCT CTC ATG GTG ATT GTG GAA Leu Gly Ala Cys Thr Lys Pro Gly Gly Pro Leu Met Val Ile Val Glu 900 905 910 915			3030
TTC TGC AAG TTT GGA AAC CTA TCA ACT TAC TTA CGG GGC AAG AGA AAT Phe Cys Lys Phe Gly Asn Leu Ser Thr Tyr Leu Arg Gly Lys Arg Asn 920 925 930			3078

GAA TTT GTT CCC TAT AAG AGC AAA GGG GCA CGC TTC CGC CAG GGC AAG Glu Phe Val Pro Tyr Lys Ser Lys Gly Ala Arg Phe Arg Gln Gly Lys 935 940 945	3126
GAC TAC GTT GGG GAG CTC TCC GTG GAT CTG AAA AGA CGC TTG GAC AGC Asp Tyr Val Gly Glu Leu Ser Val Asp Leu Lys Arg Arg Leu Asp Ser 950 955 960	3174
ATC ACC AGC AGC CAG AGC TCT GCC AGC TCA GGC TTT GTT GAG GAG AAA Ile Thr Ser Ser Gln Ser Ser Ala Ser Ser Gly Phe Val Glu Glu Lys 965 970 975	3222
TCG CTC AGT GAT GTA GAG GAA GAA GAA GCT TCT GAA GAA CTG TAC AAG Ser Leu Ser Asp Val Glu Glu Glu Glu Ala Ser Glu Glu Leu Tyr Lys 980 985 990 995	3270
GAC TTC CTG ACC TTG GAG CAT CTC ATC TGT TAC AGC TTC CAA GTG GCT Asp Phe Leu Thr Leu Glu His Leu Ile Cys Tyr Ser Phe Gln Val Ala 1000 1005 1010	3318
AAG GGC ATG GAG TTC TTG GCA TCA AGG AAG TGT ATC CAC AGG GAC CTG Lys Gly Met Glu Phe Leu Ala Ser Arg Lys Cys Ile His Arg Asp Leu 1015 1020 1025	3366
GCA GCA CGA AAC ATT CTC CTA TCG GAG AAG AAT GTG GTT AAG ATC TGT Ala Ala Arg Asn Ile Leu Leu Ser Glu Lys Asn Val Val Lys Ile Cys 1030 1035 1040	3414
GAC TTC GGC TTG GCC CGG GAC ATT TAT AAA GAC CCG GAT TAT GTC AGA Asp Phe Gly Leu Ala Arg Asp Ile Tyr Lys Asp Pro Asp Tyr Val Arg 1045 1050 1055	3462
AAA GGA GAT GCC CGA CTC CCT TTG AAG TGG ATG GCC CCG GAA ACC ATT Lys Gly Asp Ala Arg Leu Pro Leu Lys Trp Met Ala Pro Glu Thr Ile 1060 1065 1070 1075	3510
TTT GAC AGA GTA TAC ACA ATT CAG AGC GAT GTG TGG TCT TTC GGT GTG Phe Asp Arg Val Tyr Thr Ile Gln Ser Asp Val Trp Ser Phe Gly Val 1080 1085 1090	3558
TTG CTC TGG GAA ATA TTT TCC TTA GGT GCC TCC CCA TAC CCT GGG GTC Leu Leu Trp Glu Ile Phe Ser Leu Gly Ala Ser Pro Tyr Pro Gly Val 1095 1100 1105	3606
AAG ATT GAT GAA GAA TTT TGT AGG AGA TTG AAA GAA GGA ACT AGA ATG Lys Ile Asp Glu Glu Phe Cys Arg Arg Leu Lys Glu Gly Thr Arg Met 1110 1115 1120	3654
CGG GCT CCT GAC TAC ACT ACC CCA GAA ATG TAC CAG ACC ATG CTG GAC Arg Ala Pro Asp Tyr Thr Thr Pro Glu Met Tyr Gln Thr Met Leu Asp 1125 1130 1135	3702
TGC TGG CAT GAG GAC CCC AAC CAG AGA CCC TCG TTT TCA GAG TTG GTG Cys Trp His Glu Asp Pro Asn Gln Arg Pro Ser Phe Ser Glu Leu Val 1140 1145 1150 1155	3750
GAG CAT TTG GGA AAC CTC CTG CAA GCA AAT GCG CAG CAG GAT GGC AAA Glu His Leu Gly Asn Leu Leu Gln Ala Asn Ala Gln Gln Asp Gly Lys 1160 1165 1170	3798
GAC TAT ATT GTT CTT CCA ATG TCA GAG ACA CTG AGC ATG GAA GAG GAT	3846

Asp Tyr Ile Val Leu Pro Met Ser Glu Thr Leu Ser Met Glu Glu Asp	
1175 1180 1185	
TCT GGA CTC TCC CTG CCT ACC TCA CCT GTT TCC TGT ATG GAG GAA GAG	3894
Ser Gly Leu Ser Leu Pro Thr Ser Pro Val Ser Cys Met Glu Glu Glu	
1190 1195 1200	
GAA GTG TGC GAC CCC AAA TTC CAT TAT GAC AAC ACA GCA GGA ATC AGT	3942
Glu Val Cys Asp Pro Lys Phe His Tyr Asp Asn Thr Ala Gly Ile Ser	
1205 1210 1215	
CAT TAT CTC CAG AAC AGT AAG CGA AAG AGC CGG CCA GTG AGT GTA AAA	3990
His Tyr Leu Gln Asn Ser Lys Arg Lys Ser Arg Pro Val Ser Val Lys	
1220 1225 1230 1235	
ACA TTT GAA GAT ATC CCA TTG GAG GAA CCA GAA GTA AAA GTG ATC CCA	4038
Thr Phe Glu Asp Ile Pro Leu Glu Glu Pro Glu Val Lys Val Ile Pro	
1240 1245 1250	
GAT GAC AGC CAG ACA GAC AGT GGG ATG GTC CTT GCA TCA GAA GAG CTG	4086
Asp Asp Ser Gln Thr Asp Ser Gly Met Val Leu Ala Ser Glu Glu Leu	
1255 1260 1265	
AAA ACT CTG GAA GAC AGG AAC AAA TTA TCT CCA TCT TTT GGT GGA ATG	4134
Lys Thr Leu Glu Asp Arg Asn Lys Leu Ser Pro Ser Phe Gly Gly Met	
1270 1275 1280	
ATG CCC AGT AAA AGC AGG GAG TCT GTG GCC TCG GAA GGC TCC AAC CAG	4182
Met Pro Ser Lys Ser Arg Glu Ser Val Ala Ser Glu Gly Ser Asn Gln	
1285 1290 1295	
ACC AGT GGC TAC CAG TCT GGG TAT CAC TCA GAT GAC ACA GAC ACC ACC	4230
Thr Ser Gly Tyr Gln Ser Gly Tyr His Ser Asp Asp Thr Asp Thr Thr	
1300 1305 1310 1315	
GTG TAC TCC AGC GAC GAG GCA GGA CTT TTA AAG ATG GTG GAT GCT GCA	4278
Val Tyr Ser Ser Asp Glu Ala Gly Leu Leu Lys Met Val Asp Ala Ala	
1320 1325 1330	
GTT CAC GCT GAC TCA GGG ACC ACA CTG CAG CTC ACC TCC TGT TTA AAT	4326
Val His Ala Asp Ser Gly Thr Thr Leu Gln Leu Thr Ser Cys Leu Asn	
1335 1340 1345	
GGA AGT GGT CCT GTC CCG GCT CCG CCC CCA ACT CCT GGA AAT CAC GAG	4374
Gly Ser Gly Pro Val Pro Ala Pro Pro Pro Thr Pro Gly Asn His Glu	
1350 1355 1360	
AGA GGT GCT GCT TAGATTTTCA AGTGTGTGTC TTTCCACCAC CCGGAAGTAG	4426
Arg Gly Ala Ala	
1365	
CCACATTTGA TTTTCATTTT TGGAGGAGGG ACCTCAGACT GCAAGGAGCT TGTCCTCAGG	4486
GCATTTCCAG AGAAGATGCC CATGACCCAA GAATGTGTTG ACTCTACTCT CTTTTCATT	4546
CATTTAAAAG TCCTATATAA TGTGCCCTGC TGTGGTCTCA CTACCAGTTA AAGCAAAAGA	4606
CTTTCAAACA CGTGGACTCT GTCCTCCAAG AAGTGGCAAC GGCACCTCTG TGAACTGGA	4666
TCGAATGGGC AATGCTTTGT GTGTTGAGGA TGGGTGAGAT GTCCCAGGGC CGAGTCTGTC	4726

TACCTTGGAG GCTTTGTGGA GGATGCGGGC TATGAGCCAA GTGTAAAGTG TGGGATGTGG	4786
ACTGGGAGGA AGGAAGGCGC AAGTCGCTCG GAGAGCGGTT GGAGCCTGCA GATGCATTGT	4846
GCTGGCTCTG GTGGAGGTGG GCTTGTGGCC TGTCAGGAAA CGCAAAGGCG GCCGGCAGGG	4906
TTTGGTTTTG GAAGGTTTGC GTGCTCTTCA CAGTCGGGTT ACAGGCGAGT TCCCTGTGGC	4966
GTTTCCTACT CCTAATGAGA GTTCCTTCCG GACTCTTACG TGTCTCCTGG CCTGGCCCCA	5026
GGAAGGAAAT GATGCAGCTT GCTCCTTCCT CATCTCTCAG GCTGTGCCTT AATTCAGAAC	5086
ACCAAAAGAG AGGAACGTCG GCAGAGGCTC CTGACGGGGC CGAAGAATTG TGAGAACAGA	5146
ACAGAACTC AGGGTTTCTG CTGGGTGGAG ACCCACGTGG CGCCCTGGTG GCAGGTCTGA	5206
GGGTTCTCTG TCAAGTGGCG GTAAAGGCTC AGGCTGGTGT TCTTCCTCTA TCTCCACTCC	5266
TGTCAGGCCC CCAAGTCCTC AGTATTTTAG CTTTGTGGCT TCCTGATGGC AGAAAAATCT	5326
TAATTGGTTG GTTTGCTCTC CAGATAATCA CTAGCCAGAT TTCGAAATTA CTTTTTAGCC	5386
GAGGTTATGA TAACATCTAC TGTATCCTTT AGAATTTTAA CCTATAAAAC TATGTCTACT	5446
GGTTTCTGCC TGTGTGCTTA TGTT	5470

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1367 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Glu	Ser	Lys	Ala	Leu	Leu	Ala	Val	Ala	Leu	Trp	Phe	Cys	Val	Glu
1				5				10						15	
Thr	Arg	Ala	Ala	Ser	Val	Gly	Leu	Thr	Gly	Asp	Phe	Leu	His	Pro	Pro
			20				25						30		
Lys	Leu	Ser	Thr	Gln	Lys	Asp	Ile	Leu	Thr	Ile	Leu	Ala	Asn	Thr	Thr
		35					40					45			
Leu	Gln	Ile	Thr	Cys	Arg	Gly	Gln	Arg	Asp	Leu	Asp	Trp	Leu	Trp	Pro
	50					55				60					
Asn	Ala	Gln	Arg	Asp	Ser	Glu	Glu	Arg	Val	Leu	Val	Thr	Glu	Cys	Gly
65				70					75					80	
Gly	Gly	Asp	Ser	Ile	Phe	Cys	Lys	Thr	Leu	Thr	Ile	Pro	Arg	Val	Val
			85					90						95	
Gly	Asn	Asp	Thr	Gly	Ala	Tyr	Lys	Cys	Ser	Tyr	Arg	Asp	Val	Asp	Ile
	100						105					110			
Ala	Ser	Thr	Val	Tyr	Val	Tyr	Val	Arg	Asp	Tyr	Arg	Ser	Pro	Phe	Ile
	115						120					125			

Ala Ser Val Ser Asp Gln His Gly Ile Val Tyr Ile Thr Glu Asn Lys
130 135 140

Asn Lys Thr Val Val Ile Pro Cys Arg Gly Ser Ile Ser Asn Leu Asn
145 150 155 160

Val Ser Leu Cys Ala Arg Tyr Pro Glu Lys Arg Phe Val Pro Asp Gly
165 170 175

Asn Arg Ile Ser Trp Asp Ser Glu Ile Gly Phe Thr Leu Pro Ser Tyr
180 185 190

Met Ile Ser Tyr Ala Gly Met Val Phe Cys Glu Ala Lys Ile Asn Asp
195 200 205

Glu Thr Tyr Gln Ser Ile Met Tyr Ile Val Val Val Val Gly Tyr Arg
210 215 220

Ile Tyr Asp Val Ile Leu Ser Pro Pro His Glu Ile Glu Leu Ser Ala
225 230 235 240

Gly Glu Lys Leu Val Leu Asn Cys Thr Ala Arg Thr Glu Leu Asn Val
245 250 255

Gly Leu Asp Phe Thr Trp His Ser Pro Pro Ser Lys Ser His His Lys
260 265 270

Lys Ile Val Asn Arg Asp Val Lys Pro Phe Pro Gly Thr Val Ala Lys
275 280 285

Met Phe Leu Ser Thr Leu Thr Ile Glu Ser Val Thr Lys Ser Asp Gln
290 295 300

Gly Glu Tyr Thr Cys Val Ala Ser Ser Gly Arg Met Ile Lys Arg Asn
305 310 315 320

Arg Thr Phe Val Arg Val His Thr Lys Pro Phe Ile Ala Phe Gly Ser
325 330 335

Gly Met Lys Ser Leu Val Glu Ala Thr Val Gly Ser Gln Val Arg Ile
340 345 350

Pro Val Lys Tyr Leu Ser Tyr Pro Ala Pro Asp Ile Lys Trp Tyr Arg
355 360 365

Asn Gly Arg Pro Ile Glu Ser Asn Tyr Thr Met Ile Val Gly Asp Glu
370 375 380

Leu Thr Ile Met Glu Val Thr Glu Arg Asp Ala Gly Asn Tyr Thr Val
385 390 395 400

Ile Leu Thr Asn Pro Ile Ser Met Glu Lys Gln Ser His Met Val Ser
405 410 415

Leu Val Val Asn Val Pro Pro Gln Ile Gly Glu Lys Ala Leu Ile Ser
420 425 430

Pro Met Asp Ser Tyr Gln Tyr Gly Thr Met Gln Thr Leu Thr Cys Thr
435 440 445

Val Tyr Ala Asn Pro Pro Leu His His Ile Gln Trp Tyr Trp Gln Leu

450	455	460
Glu Glu Ala Cys Ser Tyr Arg Pro Gly Gln Thr Ser Pro Tyr Ala Cys 465 470 475 480		
Lys Glu Trp Arg His Val Glu Asp Phe Gln Gly Gly Asn Lys Ile Glu 485 490 495		
Val Thr Lys Asn Gln Tyr Ala Leu Ile Glu Gly Lys Asn Lys Thr Val 500 505 510		
Ser Thr Leu Val Ile Gln Ala Ala Asn Val Ser Ala Leu Tyr Lys Cys 515 520 525		
Glu Ala Ile Asn Lys Ala Gly Arg Gly Glu Arg Val Ile Ser Phe His 530 535 540		
Val Ile Arg Gly Pro Glu Ile Thr Val Gln Pro Ala Ala Gln Pro Thr 545 550 555 560		
Glu Gln Glu Ser Val Ser Leu Leu Cys Thr Ala Asp Arg Asn Thr Phe 565 570 575		
Glu Asn Leu Thr Trp Tyr Lys Leu Gly Ser Gln Ala Thr Ser Val His 580 585 590		
Met Gly Glu Ser Leu Thr Pro Val Cys Lys Asn Leu Asp Ala Leu Trp 595 600 605		
Lys Leu Asn Gly Thr Met Phe Ser Asn Ser Thr Asn Asp Ile Leu Ile 610 615 620		
Val Ala Phe Gln Asn Ala Ser Leu Gln Asp Gln Gly Asp Tyr Val Cys 625 630 635 640		
Ser Ala Gln Asp Lys Lys Thr Lys Lys Arg His Cys Leu Val Lys Gln 645 650 655		
Leu Ile Ile Leu Glu Arg Met Ala Pro Met Ile Thr Gly Asn Leu Glu 660 665 670		
Asn Gln Thr Thr Thr Ile Gly Glu Thr Ile Glu Val Thr Cys Pro Ala 675 680 685		
Ser Gly Asn Pro Thr Pro His Ile Thr Trp Phe Lys Asp Asn Glu Thr 690 695 700		
Leu Val Glu Asp Ser Gly Ile Val Leu Arg Asp Gly Asn Arg Asn Leu 705 710 715 720		
Thr Ile Arg Arg Val Arg Lys Glu Asp Gly Gly Leu Tyr Thr Cys Gln 725 730 735		
Ala Cys Asn Val Leu Gly Cys Ala Arg Ala Glu Thr Leu Phe Ile Ile 740 745 750		
Glu Gly Ala Gln Glu Lys Thr Asn Leu Glu Val Ile Ile Leu Val Gly 755 760 765		
Thr Ala Val Ile Ala Met Phe Phe Trp Leu Leu Leu Val Ile Val Leu 770 775 780		

Arg Thr Val Lys Arg Ala Asn Glu Gly Glu Leu Lys Thr Gly Tyr Leu
785 790 795 800

Ser Ile Val Met Asp Pro Asp Glu Leu Pro Leu Asp Glu Arg Cys Glu
805 810 815

Arg Leu Pro Tyr Asp Ala Ser Lys Trp Glu Phe Pro Arg Asp Arg Leu
820 825 830

Lys Leu Gly Lys Pro Leu Gly Arg Gly Ala Phe Gly Gln Val Ile Glu
835 840 845

Ala Asp Ala Phe Gly Ile Asp Lys Thr Ala Thr Cys Lys Thr Val Ala
850 855 860

Val Lys Met Leu Lys Glu Gly Ala Thr His Ser Glu His Arg Ala Leu
865 870 875 880

Met Ser Glu Leu Lys Ile Leu Ile His Ile Gly His His Leu Asn Val
885 890 895

Val Asn Leu Leu Gly Ala Cys Thr Lys Pro Gly Gly Pro Leu Met Val
900 905 910

Ile Val Glu Phe Cys Lys Phe Gly Asn Leu Ser Thr Tyr Leu Arg Gly
915 920 925

Lys Arg Asn Glu Phe Val Pro Tyr Lys Ser Lys Gly Ala Arg Phe Arg
930 935 940

Gln Gly Lys Asp Tyr Val Gly Glu Leu Ser Val Asp Leu Lys Arg Arg
945 950 955 960

Leu Asp Ser Ile Thr Ser Ser Gln Ser Ser Ala Ser Ser Gly Phe Val
965 970 975

Glu Glu Lys Ser Leu Ser Asp Val Glu Glu Glu Glu Ala Ser Glu Glu
980 985 990

Leu Tyr Lys Asp Phe Leu Thr Leu Glu His Leu Ile Cys Tyr Ser Phe
995 1000 1005

Gln Val Ala Lys Gly Met Glu Phe Leu Ala Ser Arg Lys Cys Ile His
1010 1015 1020

Arg Asp Leu Ala Ala Arg Asn Ile Leu Leu Ser Glu Lys Asn Val Val
1025 1030 1035 1040

Lys Ile Cys Asp Phe Gly Leu Ala Arg Asp Ile Tyr Lys Asp Pro Asp
1045 1050 1055

Tyr Val Arg Lys Gly Asp Ala Arg Leu Pro Leu Lys Trp Met Ala Pro
1060 1065 1070

Glu Thr Ile Phe Asp Arg Val Tyr Thr Ile Gln Ser Asp Val Trp Ser
1075 1080 1085

Phe Gly Val Leu Leu Trp Glu Ile Phe Ser Leu Gly Ala Ser Pro Tyr
1090 1095 1100

Pro Gly Val Lys Ile Asp Glu Glu Phe Cys Arg Arg Leu Lys Glu Gly

1105	1110	1115	1120
Thr Arg Met Arg	Ala Pro Asp Tyr Thr	Thr Pro Glu Met Tyr	Gln Thr
	1125	1130	1135
Met Leu Asp Cys Trp His Glu Asp	Pro Asn Gln Arg Pro Ser Phe Ser		
	1140	1145	1150
Glu Leu Val Glu His Leu Gly Asn Leu Leu Gln Ala Asn Ala Gln Gln			
	1155	1160	1165
Asp Gly Lys Asp Tyr Ile Val Leu Pro Met Ser Glu Thr Leu Ser Met			
	1170	1175	1180
Glu Glu Asp Ser Gly Leu Ser Leu Pro Thr Ser Pro Val Ser Cys Met			
	1185	1190	1195
Glu Glu Glu Glu Val Cys Asp Pro Lys Phe His Tyr Asp Asn Thr Ala			
	1205	1210	1215
Gly Ile Ser His Tyr Leu Gln Asn Ser Lys Arg Lys Ser Arg Pro Val			
	1220	1225	1230
Ser Val Lys Thr Phe Glu Asp Ile Pro Leu Glu Glu Pro Glu Val Lys			
	1235	1240	1245
Val Ile Pro Asp Asp Ser Gln Thr Asp Ser Gly Met Val Leu Ala Ser			
	1250	1255	1260
Glu Glu Leu Lys Thr Leu Glu Asp Arg Asn Lys Leu Ser Pro Ser Phe			
	1265	1270	1275
Gly Gly Met Met Pro Ser Lys Ser Arg Glu Ser Val Ala Ser Glu Gly			
	1285	1290	1295
Ser Asn Gln Thr Ser Gly Tyr Gln Ser Gly Tyr His Ser Asp Asp Thr			
	1300	1305	1310
Asp Thr Thr Val Tyr Ser Ser Asp Glu Ala Gly Leu Leu Lys Met Val			
	1315	1320	1325
Asp Ala Ala Val His Ala Asp Ser Gly Thr Thr Leu Gln Leu Thr Ser			
	1330	1335	1340
Cys Leu Asn Gly Ser Gly Pro Val Pro Ala Pro Pro Pro Thr Pro Gly			
	1345	1350	1355
Asn His Glu Arg Gly Ala Ala			
	1365		

(3) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GTCATGGATC TTCGTTAA

18

(4) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TTGTACAAGT ATAAGTAGTA GCCCAGGTAC CAG

33

(5) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 806 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met	Glu	Ser	Lys	Ala	Leu	Leu	Ala	Val	Ala	Leu	Trp	Phe	Cys	Val	Glu	1	5	10	15
Thr	Arg	Ala	Ala	Ser	Val	Gly	Leu	Thr	Gly	Asp	Phe	Leu	His	Pro	Pro	20	25	30	
Lys	Leu	Ser	Thr	Gln	Lys	Asp	Ile	Leu	Thr	Ile	Leu	Ala	Asn	Thr	Thr	35	40	45	
Leu	Gln	Ile	Thr	Cys	Arg	Gly	Gln	Arg	Asp	Leu	Asp	Trp	Leu	Trp	Pro	50	55	60	
Asn	Ala	Gln	Arg	Asp	Ser	Glu	Glu	Arg	Val	Leu	Val	Thr	Glu	Cys	Gly	65	70	75	80
Gly	Gly	Asp	Ser	Ile	Phe	Cys	Lys	Thr	Leu	Thr	Ile	Pro	Arg	Val	Val	85	90	95	
Gly	Asn	Asp	Thr	Gly	Ala	Tyr	Lys	Cys	Ser	Tyr	Arg	Asp	Val	Asp	Ile	100	105	110	
Ala	Ser	Thr	Val	Tyr	Val	Tyr	Val	Arg	Asp	Tyr	Arg	Ser	Pro	Phe	Ile	115	120	125	

Ala Ser Val Ser Asp Gln His Gly Ile Val Tyr Ile Thr Glu Asn Lys
130 135 140

Asn Lys Thr Val Val Ile Pro Cys Arg Gly Ser Ile Ser Asn Leu Asn
145 150 155 160

Val Ser Leu Cys Ala Arg Tyr Pro Glu Lys Arg Phe Val Pro Asp Gly
165 170 175

Asn Arg Ile Ser Trp Asp Ser Glu Ile Gly Phe Thr Leu Pro Ser Tyr
180 185 190

Met Ile Ser Tyr Ala Gly Met Val Phe Cys Glu Ala Lys Ile Asn Asp
195 200 205

Glu Thr Tyr Gln Ser Ile Met Tyr Ile Val Val Val Val Gly Tyr Arg
210 215 220

Ile Tyr Asp Val Ile Leu Ser Pro Pro His Glu Ile Glu Leu Ser Ala
225 230 235 240

Gly Glu Lys Leu Val Leu Asn Cys Thr Ala Arg Thr Glu Leu Asn Val
245 250 255

Gly Leu Asp Phe Thr Trp His Ser Pro Pro Ser Lys Ser His His Lys
260 265 270

Lys Ile Val Asn Arg Asp Val Lys Pro Phe Pro Gly Thr Val Ala Lys
275 280 285

Met Phe Leu Ser Thr Leu Thr Ile Glu Ser Val Thr Lys Ser Asp Gln
290 295 300

Gly Glu Tyr Thr Cys Val Ala Ser Ser Gly Arg Met Ile Lys Arg Asn
305 310 315 320

Arg Thr Phe Val Arg Val His Thr Lys Pro Phe Ile Ala Phe Gly Ser
325 330 335

Gly Met Lys Ser Leu Val Glu Ala Thr Val Gly Ser Gln Val Arg Ile
340 345 350

Pro Val Lys Tyr Leu Ser Tyr Pro Ala Pro Asp Ile Lys Trp Tyr Arg
355 360 365

Asn Gly Arg Pro Ile Glu Ser Asn Tyr Thr Met Ile Val Gly Asp Glu
370 375 380

Leu Thr Ile Met Glu Val Thr Glu Arg Asp Ala Gly Asn Tyr Thr Val
385 390 395 400

Ile Leu Thr Asn Pro Ile Ser Met Glu Lys Gln Ser His Met Val Ser
405 410 415

Leu Val Val Asn Val Pro Pro Gln Ile Gly Glu Lys Ala Leu Ile Ser
420 425 430

Pro Met Asp Ser Tyr Gln Tyr Gly Thr Met Gln Thr Leu Thr Cys Thr
435 440 445

Val Tyr Ala Asn Pro Pro Leu His His Ile Gln Trp Tyr Trp Gln Leu

450	455	460
Glu Glu Ala Cys Ser Tyr Arg Pro Gly Gln Thr Ser Pro Tyr Ala Cys 465 470 475 480		
Lys Glu Trp Arg His Val Glu Asp Phe Gln Gly Gly Asn Lys Ile Glu 485 490 495		
Val Thr Lys Asn Gln Tyr Ala Leu Ile Glu Gly Lys Asn Lys Thr Val 500 505 510		
Ser Thr Leu Val Ile Gln Ala Ala Asn Val Ser Ala Leu Tyr Lys Cys 515 520 525		
Glu Ala Ile Asn Lys Ala Gly Arg Gly Glu Arg Val Ile Ser Phe His 530 535 540		
Val Ile Arg Gly Pro Glu Ile Thr Val Gln Pro Ala Ala Gln Pro Thr 545 550 555 560		
Glu Gln Glu Ser Val Ser Leu Leu Cys Thr Ala Asp Arg Asn Thr Phe 565 570 575		
Glu Asn Leu Thr Trp Tyr Lys Leu Gly Ser Gln Ala Thr Ser Val His 580 585 590		
Met Gly Glu Ser Leu Thr Pro Val Cys Lys Asn Leu Asp Ala Leu Trp 595 600 605		
Lys Leu Asn Gly Thr Met Phe Ser Asn Ser Thr Asn Asp Ile Leu Ile 610 615 620		
Val Ala Phe Gln Asn Ala Ser Leu Gln Asp Gln Gly Asp Tyr Val Cys 625 630 635 640		
Ser Ala Gln Asp Lys Lys Thr Lys Lys Arg His Cys Leu Val Lys Gln 645 650 655		
Leu Ile Ile Leu Glu Arg Met Ala Pro Met Ile Thr Gly Asn Leu Glu 660 665 670		
Asn Gln Thr Thr Thr Ile Gly Glu Thr Ile Glu Val Thr Cys Pro Ala 675 680 685		
Ser Gly Asn Pro Thr Pro His Ile Thr Trp Phe Lys Asp Asn Glu Thr 690 695 700		
Leu Val Glu Asp Ser Gly Ile Val Leu Arg Asp Gly Asn Arg Asn Leu 705 710 715 720		
Thr Ile Arg Arg Val Arg Lys Glu Asp Gly Gly Leu Tyr Thr Cys Gln 725 730 735		
Ala Cys Asn Val Leu Gly Cys Ala Arg Ala Glu Thr Leu Phe Ile Ile 740 745 750		
Glu Gly Ala Gln Glu Lys Thr Asn Leu Glu Val Ile Ile Leu Val Gly 755 760 765		
Thr Ala Val Ile Ala Met Phe Phe Trp Leu Leu Leu Val Ile Val Leu 770 775 780		

Arg Thr Val Lys Arg Ala Asn Glu Gly Glu Leu Lys Thr Gly Tyr Leu
785 790 795 800

Ser Ile Val Met Asp Pro

(6) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 180 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ile	Leu	Ile	His	Ile	Gly	His	His	Leu	Asn	Val	Val	Asn	Leu	Leu	Gly	
1				5					10						15	
Ala	Cys	Thr	Lys	Pro	Gly	Gly	Pro	Leu	Met	Val	Ile	Val	Glu	Phe	Cys	
			20					25					30			
Lys	Phe	Gly	Asn	Leu	Ser	Thr	Tyr	Leu	Arg	Gly	Lys	Arg	Asn	Glu	Phe	
		35					40					45				
Val	Pro	Tyr	Lys	Ser	Lys	Gly	Ala	Arg	Phe	Arg	Gln	Gly	Lys	Asp	Tyr	
	50					55					60					
Val	Gly	Glu	Leu	Ser	Val	Asp	Leu	Lys	Arg	Arg	Leu	Asp	Ser	Ile	Thr	
65				70					75					80		
Ser	Ser	Gln	Ser	Ser	Ala	Ser	Ser	Gly	Phe	Val	Glu	Glu	Lys	Ser	Leu	
			85						90					95		
Ser	Asp	Val	Glu	Glu	Glu	Glu	Ala	Ser	Glu	Glu	Leu	Tyr	Lys	Asp	Phe	
		100						105						110		
Leu	Thr	Leu	Glu	His	Leu	Ile	Cys	Tyr	Ser	Phe	Gln	Val	Ala	Lys	Gly	
		115					120					125				
Met	Glu	Phe	Leu	Ala	Ser	Arg	Lys	Cys	Ile	His	Arg	Asp	Leu	Ala	Ala	
	130					135					140					
Arg	Asn	Ile	Leu	Leu	Ser	Glu	Lys	Asn	Val	Val	Lys	Ile	Cys	Asp	Phe	
145				150						155				160		
Gly	Leu	Ala	Arg	Asp	Ile	Tyr	Lys	Asp	Pro	Asp	Tyr	Val	Arg	Lys	Gly	
			165					170						175		
Asp	Ala	Arg	Leu													
			180													